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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/142,108C

DATE: 05/16/2002 P.6
 TIME: 16:07:34

Input Set : A:\11658.asc
 Output Set: N:\CRF3\05162002\I142108C.raw

4 <110> APPLICANT: Brugliera, Filippa
 5 Holton, Timothy A.
 6 Michael, Michael Z.
 8 <120> TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
 9 AND USES THEREFOR
 11 <130> FILE REFERENCE: 11658
 13 <140> CURRENT APPLICATION NUMBER: 09/142,108C
 14 <141> CURRENT FILING DATE: 1998-09-01
 16 <150> PRIOR APPLICATION NUMBER: PN8386
 17 <151> PRIOR FILING DATE: 1996-03-01
 19 <160> NUMBER OF SEQ ID NOS: 45
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1789
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Petunia x hybrida
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (50)..(1588)
 32 <400> SEQUENCE: 1
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 34 Met Glu Ile
 35 1
 37 tta agc cta att ctg tac acc gtc att ttc tca ttt ctt cta caa ttc 106
 38 Leu Ser Leu Ile Leu Tyr Thr Val Ile Phe Ser Phe Leu Leu Gln Phe
 39 5 10 15
 41 att ctt aga tca ttt ttc cgt aaa cgt tac cct tta cca tca cca cca 154
 42 Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro Leu Pro Pro
 43 20 25 30 35
 45 ggt cca aaa cca tgg cca att ata gga aac cta gtc cat ctt gga ccc 202
 46 Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His Leu Gly Pro
 47 40 45 50
 49 aaa cca cat caa tca act gca gcc atg gct caa act tat gga cca ctc 250
 50 Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr Gly Pro Leu
 51 55 60 65
 53 atg tat ctt aag atg ggg ttc gta gac gtc gtc gtt gca gcc tcg gca 298
 54 Met-Tyr-Leu-Lys-Met-Gly-Phe-Val-Asp-Val-Val-Ala-Ala-Ser-Ala
 55 70 75 80
 57 tcg gtt gca gct cag ttc ttg aaa act cat gat gct aat ttc tcg agc 346
 58 Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn Phe Ser Ser
 59 85 90 95
 61 cgt cca cca aat tct ggt gca gaa cat atg gct tat aat tat cag gat 394
 62 Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn Tyr Gln Asp

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63	100	105	110	115													
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66	Leu	Val	Phe	Ala	Pro	Tyr	Gly	Pro	Arg	Trp	Arg	Met	Leu	Arg	Lys	Ile	
67																130	
69	tgc	tca	gtt	cac	ctt	ttc	tct	acc	aag	gct	tta	gat	gac	ttc	cgc	cat	490
70	Cys	Ser	Val	His	Leu	Phe	Ser	Thr	Lys	Ala	Leu	Asp	Asp	Phe	Arg	His	
71																145	
73	gtc	cgc	cag	gat	gaa	gtg	aaa	aca	ctg	acg	cgc	gca	cta	gca	agt	gca	538
74	Val	Arg	Gln	Asp	Glu	Val	Lys	Thr	Leu	Thr	Arg	Ala	Leu	Ala	Ser	Ala	
75																160	
77	ggc	caa	aag	cca	gtc	aaa	tta	ggt	cag	tta	ttg	aac	gtg	tgc	acg	acg	586
78	Gly	Gln	Lys	Pro	Val	Lys	Leu	Gly	Gln	Leu	Leu	Asn	Val	Cys	Thr	Thr	
79																175	
81	aac	gca	ctc	gcg	cga	gta	atg	cta	ggt	aag	cga	gta	ttt	gcc	gac	gga	634
82	Asn	Ala	Leu	Ala	Arg	Val	Met	Leu	Gly	Lys	Arg	Val	Phe	Ala	Asp	Gly	
83	180															195	
85	agt	ggc	gat	gtt	gat	cca	caa	gcg	gcg	gag	ttc	aag	tca	atg	gtg	gtg	682
86	Ser	Gly	Asp	Val	Asp	Pro	Gln	Ala	Ala	Glu	Phe	Lys	Ser	Met	Val	Val	
87																210	
89	gaa	atg	atg	gta	gtc	gcc	ggt	gtt	ttt	aac	att	ggt	gat	ttt	att	ccg	730
90	Glu	Met	Met	Val	Val	Ala	Gly	Val	Phe	Asn	Ile	Gly	Asp	Phe	Ile	Pro	
91																225	
93	caa	ctt	aat	tgg	tta	gat	att	caa	ggt	gta	gcc	gct	aaa	atg	aag	aag	778
94	Gln	Leu	Asn	Trp	Leu	Asp	Ile	Gln	Gly	Val	Ala	Ala	Lys	Met	Lys	Lys	
95																240	
97	ctc	cac	gct	ttc	gac	gct	ttc	ttg	act	gat	ata	ctt	gaa	gag	cat	826	
98	Leu	His	Ala	Arg	Phe	Asp	Ala	Phe	Leu	Thr	Asp	Ile	Leu	Glu	Glu	His	
99																255	
101	aag	ggt	aaa	att	ttt	gga	gaa	atg	aaa	gat	ttg	ttg	agt	act	ttg	atc	874
102	Lys	Gly	Lys	Ile	Phe	Gly	Glu	Met	Lys	Asp	Leu	Leu	Ser	Thr	Leu	Ile	
103	260															275	
105	tct	ctt	aaa	aat	gat	gat	gct	aat	gat	gga	ggg	aaa	ctc	act	gat	922	
106	Ser	Leu	Lys	Asn	Asp	Asp	Ala	Asp	Asn	Asp	Gly	Gly	Lys	Leu	Thr	Asp	
107																290	
109	aca	gaa	att	aaa	gca	tta	ctt	ttg	aac	ttg	ttt	gta	gct	gga	aca	gac	970
110	Thr	Glu	Ile	Lys	Ala	Leu	Leu	Asn	Leu	Phe	Val	Ala	Gly	Thr	Asp		
111																305	
113	aca	tct	tct	agt	aca	gtt	gaa	tgg	gcc	att	gct	gag	ctt	att	cgt	aat	1018
114	Thr	Ser	Ser	Ser	Thr	Val	Glu	Trp	Ala	Ile	Ala	Glu	Leu	Ile	Arg	Asn	
115																320	
117	cca	aaa	ata	cta	gcc	caa	gcc	cag	caa	gag	atc	gac	aaa	gtc	gtt	gga	1066
118	Pro	Lys	Ile	Leu	Ala	Gln	Ala	Gln	Gln	Glu	Ile	Asp	Lys	Val	Val	Gly	
119																335	
121	agg	gac	cg	cta	gtt	ggc	gaa	ttt	gac	ctt	gaa	ttt	aca	tac	ttt		1114
123	Arg	Asp	Arg	Leu	Val	Gly	Glu	Leu	Asp	Leu	Ala	Gln	Leu	Thr	Tyr	Leu	
124	340															355	
126	gaa	gct	ata	gtc	aag	gaa	acc	ttt	cg	ttt	cat	cca	tca	acc	cct	355	1162
127	Glu	Ala	Ile	Val	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	Ser	Thr	Pro	Leu	
128																370	

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Input Set : A:\11658.asc
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130	tca	ctt	cct	aga	att	gca	tct	gag	agt	tgt	gag	atc	aat	ggc	tat	ttc	1210
131	Ser	Leu	Pro	Arg	Ile	Ala	Ser	Glu	Ser	Cys	Glu	Ile	Asn	Gly	Tyr	Phe	
132					375											385	
134	att	cca	aaa	ggc	tca	acg	ctt	ctc	ctt	aat	gtt	tgg	gcc	att	gct	cgt	1258
135	Ile	Pro	Lys	Gly	Ser	Thr	Leu	Leu	Leu	Asn	Val	Trp	Ala	Ile	Ala	Arg	
136					390											400	
138	gat	cca	aat	gca	tgg	gct	gat	cca	ttg	gag	ttt	agg	cct	gaa	agg	ttt	1306
139	Asp	Pro	Asn	Ala	Trp	Ala	Asp	Pro	Leu	Glu	Phe	Arg	Pro	Glu	Arg	Phe	
140					405											415	
142	ttg	cca	gga	ggg	gag	aag	ccc	aaa	gtt	gat	gtc	cgt	ggg	aat	gac	ttt	1354
143	Leu	Pro	Gly	Gly	Glu	Lys	Pro	Lys	Val	Asp	Val	Arg	Gly	Asn	Asp	Phe	
144					420											435	
146	gaa	gtc	ata	cca	ttt	gga	gct	gga	cgt	agg	att	tgt	gct	gga	atg	aat	1402
147	Glu	Val	Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Met	Asn	
148					440											450	
150	ttg	ggg	ata	cgt	atg	gtc	cag	ttg	atg	att	gca	act	tta	ata	cat	gca	1450
151	Leu	Gly	Ile	Arg	Met	Val	Gln	Leu	Met	Ile	Ala	Thr	Leu	Ile	His	Ala	
152					455											465	
154	ttt	aac	tgg	gat	ttg	gtc	agt	gga	caa	ttg	ccg	gag	atg	ttg	aat	atg	1498
155	Phe	Asn	Trp	Asp	Leu	Val	Ser	Gly	Gln	Leu	Pro	Glu	Met	Leu	Asn	Met	
156					470											480	
158	gaa	gaa	gca	tat	ggg	ctg	acc	tta	caa	ccg	gct	gat	cca	ttg	gtt	gtg	1546
159	Glu	Glu	Ala	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Asp	Pro	Leu	Val	Val	
160					485											495	
162	cac	cca	agg	cct	cgc	tta	gaa	gcc	caa	gcg	tac	att	ggg	tga			1588
163	His	Pro	Arg	Pro	Arg	Leu	Glu	Ala	Gln	Ala	Tyr	Ile	Gly				
164					500											510	
166	gcagcaacag	cccatggaga	taacatgagt	gttaaatgta	tgagtctcca	tatcttgttt											1648
168	agtttggat	tgcttggat	ttagtagttt	ttatattgat	agatcaatgt	ttgcattgtc											1708
170	agtaagaata	tccgttgctt	gtttcattaa	ctccagggtgg	acaataaaaag	aagtaatttg											1768
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184	Leu	Gln	Phe	Ile	Leu	Arg	Ser	Phe	Phe	Arg	Lys	Arg	Tyr	Pro	Leu	Pro	
185					20					25						30	
186	Leu	Pro	Pro	Gly	Pro	Lys	Pro	Trp	Pro	Ile	Ile	Gly	Asn	Leu	Val	His	
187					35					40						45	
188	Leu	Gly	Pro	Lys	Pro	His	Gln	Ser	Thr	Ala	Ala	Met	Ala	Gln	Thr	Tyr	
189					50					55						60	
190	Gly	Pro	Leu	Met	Tyr	Leu	Lys	Met	Gly	Phe	Val	Asp	Val	Val	Val	Ala	
191					65					70						75	
192	Ala	Ser	Ala	Ser	Val	Ala	Ala	Gln	Phe	Leu	Lys	Thr	His	Asp	Ala	Asn	
193					85					90						95	
194	Phe	Ser	Ser	Arg	Pro	Pro	Asn	Ser	Gly	Ala	Glu	His	Met	Ala	Tyr	Asn	

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196	Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu			
197	115	120	125	
198	Arg Lys Ile Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp			
199	130	135	140	
200	Phe Arg His Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu			
201	145	150	155	160
202	Ala Ser Ala Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val			
203	165	170	175	
204	Cys Thr Thr Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe			
205	180	185	190	
206	Ala Asp Gly Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser			
207	195	200	205	
208	Met Val Val Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp			
209	210	215	220	
210	Phe Ile Pro Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys			
211	225	230	235	240
212	Met Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu			
213	245	250	255	
214	Glu Glu His Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser			
215	260	265	270	
216	Thr Leu Ile Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys			
217	275	280	285	
218	Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala			
219	290	295	300	
220	Gly Thr Asp Thr Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu			
221	305	310	315	320
222	Ile Arg Asn Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys			
223	325	330	335	
224	Val Val Gly Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu			
225	340	345	350	
226	Thr Tyr Leu Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser			
227	355	360	365	
228	Thr Pro Leu Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn			
229	370	375	380	
230	Gly Tyr Phe Ile Pro Lys Gly Ser Thr Leu Leu Asn Val Trp Ala			
231	385	390	395	400
232	Ile Ala Arg Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro			
233	405	410	415	
234	Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly			
235	420	425	430	
236	Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala			
237	435	440	445	
238	Gly Met Asn Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu			
239	450	455	460	
240	Ile His Ala Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met			
241	465	470	475	480
242	Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro			
243	485	490	495	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/142,108C

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Output Set: N:\CRF3\05162002\I142108C.raw

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246 500 505 510
250 <210> SEQ_ID NO: 3
251 <211> LENGTH: 1737
252 <212> TYPE: DNA
253 <213> ORGANISM: Dianthus caryophyllus
256 <220> FEATURE:
257 <221> NAME/KEY: CDS
258 <222> LOCATION: (172)..(1674)
260 <400> SEQUENCE: 3
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263 acctctcttt tctaccacc aaaacaaaac aaaacaaaaa aaaacacata aaaaaactca 120
265 aaaaaaaaaatt ataatgtcac ccttagaggt aactttctac accatagtcc t atg cac 177
266 Met His
267 1
269 aat ctc tac tac ctc atc acc acc gtc ttc cgc ggc cac caa aaa ccg 225
270 Asn Leu Tyr Tyr Leu Ile Thr Thr Val Phe Arg Gly His Gln Lys Pro
271 5 10 15
273 ctt cct cca ggg cca cga cca tgg ccc atc gtg gga aac ctc cca cat 273
274 Leu Pro Pro Gly Pro Arg Pro Trp Pro Ile Val Gly Asn Leu Pro His
275 20 25 30
277 atg ggc cag gca ccg cac cag ggc tta gca gcc ctg gcg caa aag tat 321
278 Met Gly Gln Ala Pro His Gln Gly Leu Ala Ala Leu Ala Gln Lys Tyr
279 35 40 45 50
281 ggc cct cta ttg tat atg aga ctg ggg tac gtg gac gtt gtt gtg gcc 369
282 Gly Pro Leu Leu Tyr Met Arg Leu Gly Tyr Val Asp Val Val Ala
283 55 60 65
285 gcc tca gcg tct gta gcg acc cag ttt ctt aag aca cat gac cta aat 417
286 Ala Ser Ala Ser Val Ala Thr Gln Phe Leu Lys Thr His Asp Leu Asn
287 70 75 80
289 ttt tcg agt agg cca ccg aat tcg ggg gct aaa cac att gct tat aac 465
290 Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His Ile Ala Tyr Asn
291 85 90 95
293 tat caa gac ctt gtt ttt gca cct tat gga cct aaa tgg cgc atg ctt 513
294 Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Lys Trp Arg Met Leu
295 100 105 110
297 agg aaa att tgt tcc tta cac atg ttt tct aag gct ttg gac gat 561
298 Arg Lys Ile Cys Ser Leu His Met Phe Ser Ser Lys Ala Leu Asp Asp
299 115 120 125 130
301 ttt aga ctt gtc cgt cag gaa gaa gta tct ata ctg gta aat ggc ata 609
302 Phe Arg Leu Val Arg Gln Glu Glu Val Ser Ile Leu Val Asn Ala Ile
303 135 140 145
305 gca aaa gca gga aca aag cca gta caa cta gga caa cta ctc aac gtg 657
307 Ala Lys Ala Gly Thr Lys Pro Val Gln Leu Gly Gln Leu Leu Asn Val
308 150 155 160
310 tgc acc aca aat gcc tta tcg agg gtg atg cta ggg aag cga gtt ctc 705
311 Cys Thr Thr Asn Ala Leu Ser Arg Val Met Leu Gly Lys Arg Val Leu
312 165 170 175
314 ggt gat ggc aca ggg aaa agc gac cca aaa gcc gag gaa ttt aag gac 753

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/16/2002
PATENT APPLICATION: US/09/142,108C TIME: 16:07:35

Input Set : A:\11658.asc
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#: 34; N Pos. 3,9,12,15,18,21,24,30
Seq#: 35; Xaa Pos. 3
Seq#: 36; N Pos. 3,7,8,9,12,15,18
Seq#: 40; N Pos. 3,9,12,18,21,24,30
Seq#: 44; Xaa Pos. 8,10,15
Seq#: 45; Xaa Pos. 8,10,15,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33
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VERIFICATION SUMMARY
 PATENT APPLICATION: US/09/142,108C

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 L:965 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1005 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1009 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1013 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1017 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1033 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1041 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1049 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1053 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:2778 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31
 L:2783 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31
 L:2788 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31
 L:2793 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31
 L:2798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
 L:2824 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33
 L:2829 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33
 L:2834 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33
 L:2839 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
 L:2851 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
 L:2856 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
 L:2861 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
 L:2866 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
 L:2872 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
 L:2877 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
 L:2882 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
 L:2887 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
 L:2892 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
 L:2909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
 L:2921 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
 L:2926 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
 L:2931 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
 L:2936 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
 L:2941 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
 L:2946 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
 L:2951 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
 L:2956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
 L:3000 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
 L:3005 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
 L:3010 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/142,108C

DATE: 05/16/2002
TIME: 16:07:35

Input Set : A:\11658.asc
Output Set: N:\CRF3\05162002\I142108C.raw

L:3015 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:3020 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:3025 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:3030 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:3035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:3248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
L:3282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
L:3285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:16
L:3288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:32
L:3291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:48
L:3294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:64
L:3297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:80
L:3300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:96
L:3303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:112
L:3306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:128
L:3309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:144
L:3312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:160
L:3315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:176
L:3318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:192
L:3321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:208
L:3324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:224
L:3327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:240
L:3330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:256
L:3333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:272
L:3336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:288
L:3339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:304
L:3342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:320
L:3345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:336
L:3348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:352
L:3351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:368
L:3354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:384
L:3357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:400
L:3360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:416
L:3363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:432
L:3366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:448
L:3370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:464
L:3373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:480
L:3376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:496
L:3379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:512